Supplemental Table

Fitting of the E glycoprotein X-ray structure into the negative hand cryoEM map of dengue prM particles using the EMfit program.

a) No limit on the movement of the center of mass for each fitted E molecules

Mol[a]	*sumf*1[b] (%)	*sumf*2[b] (%)	*sumf*3[b] (%)	*-den*[c] (%)	*clash* (%)	*centx*[d] (Å)	*centy*[d] (Å)	*centz*[d] (Å)	?$_1$[e] (º)	?$_2$[e] (º)	?$_3$[e] (º)	Order of fitting[f]
Blue	46.9	53.5	46.0	1.8	0.0	31.7	6.5	219.2	89.8	148.5	105.0	1st
Blue	47.3	53.6	46.4	1.8	0.0	31.7	6.5	219.7	90.0	148.5	105.0	2nd
Blue	48.5	43.2	37.6	4.1	0.0	31.7	6.5	219.7	252.0	174.0	244.5	3rd
Red	49.6	56.2	33.9	0.0	0.0	71.9	-10.1	206.9	234.5	172.2	33.0	3rd
Red	49.7	56.4	33.2	0.0	0.0	71.4	-10.1	206.4	236.2	172.5	34.5	1st
Red	49.5	56.0	33.1	0.0	0.0	71.9	-10.1	206.4	234.2	172.2	31.5	2nd
Green	46.1	49.8	39.1	1.3	0.0	-12.0	48.4	214.5	245.0	169.5	163.5	2nd
Green	47.3	51.3	35.9	1.3	0.0	-11.5	47.9	213.5	268.2	160.2	180.0	3rd
Green	45.4	50.1	49.9	1.8	0.0	-12.0	45.9	219.0	77.2	109.8	44.5	1st

b) The position of the center of mass was restrained so that the fitted molecules did not penetrate into the viral membrane

Mol[a]	*sumf*1[b] (%)	*sumf*2[b] (%)	*sumf*3[b] (%)	*-den*[c] (%)	*clash* (%)	*centx*[d] (Å)	*centy*[d] (Å)	*centz*[d] (Å)	?$_1$[e] (º)	?$_2$[e] (º)	?$_3$[e] (º)	Order of fitting[f]
Blue	46.9	53.5	46.0	1.8	0.0	31.7	6.5	219.2	89.8	148.5	105.0	1st
Blue	46.9	53.5	46.0	1.8	0.0	31.7	6.5	219.2	89.8	148.5	105.0	2nd
Blue	47.1	41.2	45.0	7.1	0.0	31.7	5.5	220.2	89.8	151.0	104.5	3rd
Red	49.9	56.3	33.6	0.3	0.0	71.9	-10.6	206.9	250.0	168.5	46.5	3rd
Red	49.8	56.5	33.1	0.3	0.0	71.9	-10.6	206.4	249.2	168.5	45.2	1st
Red	49.8	56.5	33.1	0.3	0.0	71.9	-10.6	206.4	249.2	168.5	45.2	2nd
Green	45.6	51.4	43.0	3.0	0.0	-10.0	47.9	217.2	114.0	165.0	44.2	2nd
Green	46.1	50.9	42.7	2.8	0.0	-10.0	47.9	217.0	129.0	168.0	57.2	3rd
Green	46.4	49.7	48.8	2.3	0.0	-11.5	44.9	220.0	76.0	107.8	45.2	1st

For more details of the EMfit program parameters, see Rossmann et al. (2001).

[a] Mol "red", "blue", and "green" refer to the three independently fitted molecules

[b] *Sumf*1, *sumf*2, and *sumf*3 are the average densities of C? atoms for domains I, II, and III, respectively, expressed as a percentage of the highest density in the map.

[c] *-den* is the percentage of atoms in negative density.

[d] *Centx,centy,* and *centz* are the refined coordinates of the center of mass of the E monomer in the map. Note the consistency of the results, independent of the order of fitting.

[e] ?$_1$, ?$_2$, and ?$_3$ are the refined Eulerian angles required to rotate the atomic coordinates of E into position. Note the consistency of the results.

[f] Possible fitting procedures: 1. Blue molecule (1st), followed by Green molecule (2nd), followed by Red molecule (3rd); or 2. Red molecule (1st), followed by Blue molecule (2nd), followed by green molecule (3rd); or 3. Green molecule (1st), followed by Red molecule (2nd), followed by Blue molecule (3rd).

Note that the fits, particularly for the 3rd molecule and the red molecule, are worse than when using the positively handed map (Table I). In addition, the amount of structure in negative density (–*den*) is poor compared to the fit into the positively handed map.